WHAT IS CLAIMED IS:

1. A protein-analysis method comprising:

(A) bringing a protein into contact with at least a first disease-model cell and a second disease-model cell, respectively, wherein each of said first and second cells is located in a separate well; then

(B) determining the dynamic state of each of said cells, whereby a data set is generated for each cell; and

(C) analyzing the data set for said first cell and the data set for said second cell, to obtain information about the function of said protein.

2. A method according to claim 1, wherein said first disease-model cell and said second disease-model cell relate to the same disease model.

3. A method according claim 1, wherein the data sets of step (C) address a plurality of cell parameters.

4. A method according to claim 1, wherein said determination of the dynamic state comprises imaging each of said cells by either visible or fluorescent light, or both.

5. A method according to claim 1, wherein step (A) comprises bringing said protein into contact with a first plurality of first disease-model cells and a second plurality of second disease-model cells, respectively, and wherein said information distinguishes a subpopulation of at least one of said first and second pluralities.

6. A method according to claim 1, further comprising providing a plurality of proteins, wherein step (A) comprises bringing into contact, with N number of disease-model cells, a chosen protein from said plurality such that each of at least some of said N cells contacts a different protein from said plurality, N being an integer greater than 2.

7. A method according to claim 6, wherein more than one well receives the same protein from said plurality of proteins.

8. A method according to claim 6, wherein at least one well does not receive a protein from said plurality of proteins.

9. A method according to claim 6, wherein at least one well receives more than one protein from said plurality of proteins.

10. A method according to claim 6, wherein the data sets of step (C) address a plurality of *M* cell parameters, *M* being an integer of 1 or greater.

11. A method according to claim 10, wherein said cell parameters comprise two or more of the measured parameters enumerated in Table I.

12. A method according to claim 10, wherein a data set of step (C) is organized as an *N* x *M* array of values.

13. A method according to claim 10, wherein either said first disease-model cell or said second disease-model cell employs an oncogenesis disease model.

14. A method according to claim 10, wherein either said first disease-model cell or said second disease-model cell employs a primary immune response disease model.

15. A method according to claim 10, wherein either said first disease-model cell or said second disease-model cell employs an angiogenesis disease model.

16. An integral array of biochambers, each (i) comprising a well in which a disease-model cell is located and (ii) defining a separate, closed environment for said cell, wherein each well contains a protein and said array presents a predetermined pattern of association between wells and proteins.

17. A protein-analysis method comprising:

(A) disposing a first disease-model cell in a first well in a manner wherein at least one cell is individually observable;

(B) disposing a second disease-model cell in a second well in a manner wherein at least one cell is individually observable;

(C) bringing a protein into contact with said first and second disease-model cells;

(D) repeatedly observing the first and second disease-model cells;

(E) compiling data in the form of data sets pertaining to a change in at least one of a plurality of observable characteristics of each of the respective first and second disease-model cells, prior to and subsequent to the protein being contacted with the first and second disease-model cells; and

(F) analyzing the data sets to obtain information about the function of the protein.

18. A method according to claim 17, wherein said first disease-model cell and said second disease-model cell relate to the same disease model.

19. A method according to claim 17, further comprising adding a modifying agent.

20. A method according to claim 17, wherein steps (A) through (D) are implemented robotically, within a closed environment.

21. A method according to claim 17, wherein steps (A) through (F) are implemented robotically.

22. A method according to claim 17, wherein the step of repeatedly observing is carried out optically.

23. A method according to claim 17, wherein the observable characteristics are selected from the group consisting of cell movement, cell division, apoptosis, morphology, adherence and physiological function.

24. A method according to claim 17, wherein the observable characteristics comprise the measured parameters enumerated in Table I.

25. A method according to claim 17, further comprising means for selectively adding

a modifying agent in addition to the protein.

26. A protein-analysis apparatus comprising:

means for disposing a plurality of first disease-model cells in a first well in a manner wherein at least one of the first disease-model cells is individually observable;

means for disposing a plurality of second disease-model cells in a second well a manner wherein at least one of the second disease-model cells is individually observable;

means for bringing a protein into contact with at least one of the first and second disease-model cells;

means for repeatedly observing the first and second disease-model cells;

means for compiling and analyzing data in the form of data sets that pertain to a change in at least one of a plurality of observable characteristics of each of the respective first and second disease-model cells, prior to and subsequent to the protein being contacted with the first and second disease-model cells.

27. A protein-analysis method comprising:

(A) disposing a disease-model cell in a well in a manner wherein at least one cell is individually observable;

(B) bringing a plurality of proteins into contact with said disease-model cell;

(D) repeatedly observing said disease-model cell;

(E) compiling data in the form of data sets pertaining to a change in at least one of a plurality of observable characteristics of disease-model cell, prior to and subsequent to the proteins being contacted with the disease-model cell; and

(F) analyzing the data sets to obtain information about the function of the proteins.

28. The method of claim 27, further comprising isolating a protein of interest by splitting said plurality into a smaller number of pluralites and repeating steps (A) thru (F), using said smaller number of pluralites for step (B).

29. The method of claim 27, further comprising isolating a protein of interest by splitting said plurality into individual proteins and repeating steps (A) thru (F) for each of said proteins.